



RECEIVED

AUG 13 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Covacci, Antonio
Bugnoli, Massimo
Telford, John
Macchia, Giovanni
Rappuoli, Rino

<120> Helicobacter Pylori Cytotoxin Proteins Useful For Vaccines And Diagnostics

<130> CHIR-0315

<140> 09/921,157

<141> 2001-08-02

<150> 08/466,662

<151> 1995-06-06

<150> 08/256,848

<151> 1994-10-21

<150> 09/360,934

<151> 1999-07-26

<150> 08/471,491

<151> 1995-06-06

<150> PCT/EP93/00472

<151> 1993-03-02

<150> PCT/EP93/00158

<151> 1993-01-25

<150> FI 92 A 000052

<151> 1992-03-02

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Oligonucleotide

<400> 1

gcaagcttat cgatgtcgac tcgagct

27

<210> 2

<211> 3960

<212> DNA

<213> Helicobacter pylori

<400> 2

aaaaagaaag gaagaaaatg gaaatacaac aaacacaccg caaaatcaat cgccctctgg 60

tttctctcgc ttagtagtaga gcattagtaga gcatcacacc gcaacaaagt catgccgcct 120

ttttcacaac cgtgatcatt ccagccattg ttgggggtat cgctacaggc accgctgtag 180

gaacgggtctc agggcttctt agctgggggc tcaaacaagc cgaagaagcc aataaaaccc 240

cagataaacc cgataaagtt tggcgcatc aagcaggaaa aggctttaat gaattcccta 300

acaaggaata cgacttatac agatcccttt tatccagtaa gattgatgga gggtgggatt 360

gggggaatgc cgctaggcat tattgggtca aaggcgggca acagaataag cttgaagtgg 420

atatgaaaga cgctgtaggg acttatacct tatcagggct tagaaacttt actggtgggg 480

atttagatgt caatatgcaa aaagccactt tacgcttggg ccaattcaat ggcaattctt 540
 ttacaagcta taaggatagt gctgatcgca ccacgagagt ggatttcaac gctaaaaata 600
 tctcaattga taatttttga gaaatcaaca atcgtgtggg ttctggagcc gggaggaaag 660
 ccagctctac ggttttgact ttgcaagctt cagaagggat cactagcgat aaaaacgctg 720
 aaatttctct ttatgatggg gccacgctca atttggcttc aagcagcgtt aaattaatgg 780
 gtaatgtgtg gatgggccgt ttgcaatacg tgggagcgta tttggcccct tcatacagca 840
 cgataaacac ttcaaaagta acaggggaag tgaattttta ccacctcact gttggcgata 900
 aaaacgccgc tcaagcgggc attatcgcta ataaaaagac taatattggc acactggatt 960
 tgtggcaaag cgccgggtta aacattatcg ctctccaga aggtggctat aaggataaac 1020
 ccaataatac cccttctcaa agtgggtgcta aaaacgacaa aaatgaaagc gctaaaaacg 1080
 acaacaaga gagcagtcaa aataatagta acactcaggt cattaacca cccaatagtg 1140
 cgcaaaaaac agaagttcaa ccacgcaag tcattgatgg gccttttgcg ggcggaag 1200
 acacggttgt caatatcaac cgcatcaaca ctaacgctga tggcacgatt agagtgggag 1260
 ggtttaaaagc ttctcttacc accaatgcggt ctcatgtgca tatcggaac ggcggtgtca 1320
 atctgtccaa tcaagcgagc gggcgctctc ttatagtga aaatctaact gggaatatca 1380
 ccgttgatgg gcctttaaga gtgaataatc aagtgggtgg ctatgctttg gcaggatcaa 1440
 gcgcgaattt tgagtttaag gctggtacgg ataccaaaaa cggcacagcc acttttaata 1500
 acgatattag tctgggaaga tttgtgaatt taaaggtgga tgctcataca gctaatttta 1560
 aaggtattga tacgggtaat ggtggtttca acaccttaga ttttagtggc gttacagaca 1620
 aagtcaatat caacaagctc attacggctt ccactaatgt ggccgttaaa aacttcaaca 1680
 ttaatgaatt gattgttaaa accaatggga taagtgtggg ggaatatact catttttagcg 1740
 aagatatagg cagtcaatcg cgcatcaata ccgtgcgttt ggaaactggc actaggtcac 1800
 ttttctctgg ggggtgttaaa tttaaaggtg gcgaaaaatt ggttatagat gagttttact 1860
 atagcccttg gaattatttt gacgctagaa atattaaaaa tgttgaaatc accaataaac 1920
 ttgcttttgg acctcaagga agtccttggg gcacatcaaa acttatgttc aataatctaa 1980
 ccctaggtca aaatgcgggtc atggattata gccaattttc aaatttaacc attcaagggg 2040
 atttcatcaa caatcaaggc actatcaact atctggtccg aggtgggaaa gtggcaacct 2100
 taagcgtagg caatgcagca gctatgatgt ttaataatga tatagacagc gcgaccggat 2160
 tttaaaaacc gctcatcaag attaacagcg ctcaagatct cattaaaaat acagaacatg 2220
 ttttattgaa agcgaaaatc attggttatg gtaatgtttc tacaggtacc aatggcatta 2280
 gtaatgttaa tctagaagag caattcaaag agcgcctagc cttttataac aacaataacc 2340
 gcattgatac ttgtgtggtg cgaaatactg atgacattaa agcatgcggt atggctatcg 2400
 gcgatcaaag catggtgaac aaccctgaca attacaagta tcttatcggg aaggcatgga 2460
 aaaatatagg gatcagcaaa acagctaagt gctctaaaat ttcggtgtat tatttaggca 2520
 attctacgcc tactgagaat ggtggcaata ccacaaattt acccaciaac accactagca 2580
 atgcacgttc tgccaacaac gcccttgac aaaacgctcc ttcgctcaa cctagtgtca 2640

ctccctaattt agtcgctatc aatcagcatg attttggcac tattgaaagc gtgtttgaat 2700
 tggctaaccg ctctaaagat attgacacgc tttatgctaa ctcaggcgct caaggcaggg 2760
 atctctttaca aaccttattg attgatagcc atgatgcggg ttatgccaga aaaatgattg 2820
 atgctacaag cgctaataa atcaccaagc aattgaatac ggccactacc actttaaaaca 2880
 acatagccag tttagagcat aaaaccagcg gcttacaaac tttgagcttg agtaatgcga 2940
 tgattttaaa ttctcgttta gtcaatctct ccaggagaca caccaacat attgactcgt 3000
 tcgccaaacg cttacaagct taaaagacc aaaaattcgc ttcttttagaa agcgcggcag 3060
 aagtgttgta tcaatttgcc cctaaatatg aaaaacctac caatgtttgg gctaacgcta 3120
 ttgggggaac gagcttgaat aatggctcta acgcttcatt gtatggcaca agcgcgggcg 3180
 tagacgctta ccttaacggg caagtggaag ccattgtggg cggttttgga agctatggtt 3240
 atagctcttt taataatcgt gcgaactccc ttaactctgg ggccaataac actaattttg 3300
 gcgtgtatag ccgtattttt gcccaaccagc atgaatttga ctttgaagct caagggggcac 3360
 tagggagcga tcaatcaagc ttgaatttca aaagcgctct attacaagat ttgaatcaaa 3420
 gctatcatta cttagcctat agcgctgcaa caagagcgag ctatggttat gacttcgcgt 3480
 tttttaggaa cgcttttagtg ttaaaaccaa gcgtgggtgt gagctataac catttaggtt 3540
 caaccaactt taaaagcaac agcaccaatc aagtggcttt gaaaaatggc tctagcagtc 3600
 agcatttatt caacgctagc gctaattgtg aagcgcgcta ttattatggg gacacttcat 3660
 acttctacat gaatgctgga gttttacaag agttcgctca tgttggctct aataacgccg 3720
 cgtctttaaa cacctttaaa gtgaatgccg ctcgcaacct tttaaatacc catgccagag 3780
 tgatgatggg tggggaatta aaattagcta aagaagtgtt tttgaatttg ggcgttggtt 3840
 atttgcacaa tttgatttcc aatataggcc atttcgcttc caatttagga atgaggtata 3900
 gtttctaaat accgctctta aacctatgct caaagcatgg gtttgaaatc ttacaaaaca 3960

<210> 3
 <211> 1296
 <212> PRT
 <213> Helicobacter pylori
 <400> 3

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1 5 10 15

Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
20 25 30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys

85

90

95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr
130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
165 170 175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
210 215 220

Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn
245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
275 280 285

His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala
290 295 300

Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
325 330 335

Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala
340 345 350

Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val
355 360 365

Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln
370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile
385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe
405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu
435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
485 490 495

β_2 Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
500 505 510

Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr
580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu
595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg
610 615 620

Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln
625 630 635 640

Gly Ser Pro Trp Gly Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu
645 650 655

Gly Gln Asn Ala Val Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile
660 665 670

Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg
 675 680 685
 Gly Gly Lys Val Ala Thr Leu Ser Val Gly Asn Ala Ala Ala Met Met
 690 695 700
 Phe Asn Asn Asp Ile Asp Ser Ala Thr Gly Phe Tyr Lys Pro Leu Ile
 705 710 715 720
 Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys Asn Thr Glu His Val Leu
 725 730 735
 Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn Val Ser Thr Gly Thr Asn
 740 745 750
 Gly Ile Ser Asn Val Asn Leu Glu Glu Gln Phe Lys Glu Arg Leu Ala
 755 760 765
 Leu Tyr Asn Asn Asn Asn Arg Met Asp Thr Cys Val Val Arg Asn Thr
 770 775 780
 Asp Asp Ile Lys Ala Cys Gly Met Ala Ile Gly Asp Gln Ser Met Val
 785 790 795 800
 Asn Asn Pro Asp Asn Tyr Lys Tyr Leu Ile Gly Lys Ala Trp Lys Asn
 805 810 815
 Ile Gly Ile Ser Lys Thr Ala Asn Gly Ser Lys Ile Ser Val Tyr Tyr
 820 825 830
 Leu Gly Asn Ser Thr Pro Thr Glu Asn Gly Gly Asn Thr Thr Asn Leu
 835 840 845
 Pro Thr Asn Thr Thr Ser Asn Ala Arg Ser Ala Asn Asn Ala Leu Ala
 850 855 860
 Gln Asn Ala Pro Phe Ala Gln Pro Ser Ala Thr Pro Asn Leu Val Ala
 865 870 875 880
 Ile Asn Gln His Asp Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala
 885 890 895
 Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln
 900 905 910
 Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly
 915 920 925
 Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys
 930 935 940
 Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu
 945 950 955 960

His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile
 965 970 975

Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile
 980 985 990

Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala
 995 1000 1005

Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys
 1010 1015 1020

Tyr Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr
 1025 1030 1035

Ser Leu Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala
 1040 1045 1050

Gly Val Asp Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly
 1055 1060 1065

Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn
 1070 1075 1080

Ser Leu Asn Ser Gly Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser
 1085 1090 1095

Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala Gln Gly
 1100 1105 1110

Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Ala Leu
 1115 1120 1125

Leu Gln Asp Leu Asn Gln Ser Tyr His Tyr Leu Ala Tyr Ser Ala
 1130 1135 1140

Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn
 1145 1150 1155

Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu
 1160 1165 1170

Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn Gln Val Ala Leu
 1175 1180 1185

Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn
 1190 1195 1200

Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met
 1205 1210 1215

Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn Asn
 1220 1225 1230

Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro

1235

1240

1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu
1250 1255 1260

Ala Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn
1265 1270 1275

Leu Ile Ser Asn Ile Gly His Phe Ala Ser Asn Leu Gly Met Arg
1280 1285 1290

Tyr Ser Phe
1295

<210> 4
<211> 5925
<212> DNA
<213> Helicobacter pylori

<400> 4
ctccatttta agcaactcca tagaccacta aagaaacttt ttttgaggct atctttgaaa 60
atctgtccta ttgatttggt ttccattttg ttcccatgt ggatcttggt gatcaciaaac 120
gcttaattat acatgctata gtaagcatga cacacaaacc aaactatatt tagaacgctt 180
catgtgctca ccttgactaa ccatctctcc aaccatactt tagcgttgca tttgatttct 240
tcaaaaagat tcatctctta tttcttggtc ttattaaagt tctttcattt tagcaaat 300
ttgttaattg tgggtaaaaa tgtgaatcgt cctagccttt agacgcctgc aacgatcggg 360
cttttttcaa tattaataat gattaatgaa aaaaaaaaaa aatgcttgat attgttgat 420
aatgagaatg ttcaaagaca tgaattgact actcaagcgt gtagcgattt ttagcagtct 480
ttgacactaa caagataccg ataggtatga aactaggtat agtaaggaga aacaatgact 540
aacgaaacca ttgaccaaca accacaaacc gaagcggcct ttaacccgca gcaatttatc 600
aataatcttc aagtagcttt tcttaaagtt gataacgctg tcgcttcata cgatcctgat 660
caaaaaccaa tcgttgataa gaacgatagg gataacaggc aagcttttga aggaatctcg 720
caattaaggg aagaatactc caataaagcg atcaaaaatc ctacaaaaa gaatcagtat 780
ttttcagact ttatcaataa gagcaatgat ttaatcaaca aagacaatct cattgatgta 840
gaatcttcca caaagagctt tcagaaat 900
tgggtgtccc atcaaaacga tccgtctaaa atcaacaccc gatcgatccg aaattttatg 960
gaaaatatca tacaaccccc tatccttgat gataaagaga aagcggagtt tttgaaatct 1020
gccaaacaat cttttgcagg aatcattata gggaatcaaa tccgaacgga tcaaaagttc 1080
atgggcgtgt ttgatgagtc cttgaaagaa aggcaagaag cagaaaaaaa tggagagcct 1140
actggtgggg attggttgga tatttttctc tcatcttatat ttgacaaaaa acaatcttct 1200
gatgtcaaag aagcaatcaa tcaagaacca gttcccatg tccaaccaga tatagccact 1260
accaccaccg acatacaagg cttaccgcct gaagctagag atttacttga tgaaaggggt 1320
aatttttcta aattcactct tggcgatatg gaaatgttag atgttgagg agtcgctgac 1380
attgatccca attacaagtt caatcaatta ttgattcaca ataacgctct gtcttctgtg 1440

ttaatgggga gtcataatgg catagaacct gaaaaagttt cattgttgta tgggggcaat 1500
 ggtggtcctg gagctaggca tgattggaac gccaccgttg gttataaaga ccaacaaggc 1560
 aacaatgtgg ctacaataat taatgtgcat atgaaaaacg gcagtggcctt agtcatagca 1620
 ggtggtgaga aagggattaa caaccctagt ttttatctct acaaagaaga ccaactcaca 1680
 ggctcacaaac gagcattaag tcaagaagag atccaaaaca aaatagattt catggaattt 1740
 cttgcacaaa ataatgctaa attagacaac ttgagcgaga aagagaagga aaaattccga 1800
 actgagatta aagatttcca aaaagactct aaggcttatt tagacgccct aggggaatgat 1860
 cgtattgctt ttgtttctaa aaaagacaca aaacattcag ctttaattac tgagtttggt 1920
 aatgggggatt tgagctacac tctcaaagat tatgggaaaa aagcagataa agctttagat 1980
 agggagaaaa atgttactct tcaaggtagc ctaaaacatg atggcgtgat gtttgttgat 2040
 tattctaatt tcaaatacac caacgcctcc aagaatccca ataagggtgt aggcgttacg 2100
 aatggcgctt cccattttaga agtaggcttt aacaaggtag ctatctttaa tttgcctgat 2160
 ttaaataatc tcgctatcac tagtttcgta aggcggaatt tagaggataa actaaccact 2220
 aaaggattgt ccccaacaaga agctaataag cttatcaaag attttttgag cagcaacaaa 2280
 gaattggttg gaaaaacttt aaacttcaat aaagctgtag ctgacgctaa aaacacaggc 2340
 aattatgatg aagtgaaaaa agctcagaaa gatcttgaaa aatctctaag gaaacgagag 2400
 catttagaga aagaagtaga gaaaaaattg gagagcaaaa gcggcaacaa aaataaaatg 2460
 gaagcaaaaag ctcaagctaa cagccaaaaa gatgagattt ttgcgttgat caataaagag 2520
 gctaatagag acgcaagagc aatcgcttac gctcagaatc ttaaaggcat caaaagggaa 2580
 ttgtctgata aacttgaaaa tgtcaacaag aatttgaaaag actttgataa atcttttgat 2640
 gaattcaaaa atggcaaaaa taaggatttc agcaaggcag aagaaacact aaaagccctt 2700
 aaagggttcg tgaaagattt aggtatcaat ccagaatgga tttcaaaagt tgaaaacctt 2760
 aatgcagctt tgaatgaatt caaaaatggc aaaaataagg atttcagcaa ggtaacgcaa 2820
 gcaaaaagcg accttgaaaa ttccgttaaa gatgtgatca tcaatcaaaa ggtaacggat 2880
 aaagttgata atctcaatca agcgggtatca gtggctaaag caacgggtga tttcagtagg 2940
 gtagagcaag cgtttagccga tctcaaaaat ttctcaaagg agcaattggc ccaacaagct 3000
 caaaaaaatg aaagtctcaa tgctagaaaa aaatctgaaa tatatcaatc cgttaagaat 3060
 ggtgtgaatg gaaccctagt cggtaatggg ttatctcaag cagaagccac aactctttct 3120
 aaaaactttt cggacatcaa gaaagagttg aatgcaaaac ttggaaattt caataacaat 3180
 aacaataatg gactcaaaaa cgaaccattt tatgctaaag ttaataaaaa gaaagcaggg 3240
 caagcagcta gccttgaaaga acccattttac gctcaagttg ctaaaaaggt aaatgcaaaa 3300
 attgaccgac tcaatcaaat agcaagtggg ttgggtggtg tagggcaagc agcgggcttc 3360
 cctttgaaaa ggcatgataa agttgatgat ctcaagtaagg tagggctttc aaggaatcaa 3420
 gaattggctc agaaaattga caatctcaat caagcggatc cagaagctaa agcaggtttt 3480
 tttggcaatc tagagcaaac gatagacaag ctcaaagatt ctacaaaaca caatcccatg 3540
 aatctatggg ttgaaagtgc aaaaaaagta cctgctagtt tgctagcgaa actagacaat 3600
 tacgtacta acagccacat acgcattaat agcaatatca aaaatggagc aatcaatgaa 3660

aaagcgaccg gcatgctaac gcaaaaaaac cctgagtggc tcaagctcgt gaatgataag 3720
 atagttgcgc ataatgtagg aagcgttcct ttgtcagagt atgataaaat tggcttcaac 3780
 cagaagaata tgaaagatta ttctgattcg ttcaagtttt ccaccaagtt gaacaatgct 3840
 gtaaaagaca ctaattctgg ctttacgcaa tttttaacca atgcattttc tacagcatct 3900
 tattactgct tggcgagaga aaatgcggag catggaatca agaacgtaa taaaaaggt 3960
 ggtttccaaa aatctttaaag gattaaggaa taccaaaaac gcaaaaacca ccccttgcta 4020
 aaagcgaggg gttttttaat actccttagc agaaatccca atcgtcttta gtatttgga 4080
 tgaatgctac caattcatgg tatcatatcc ccatacattc gtatctagcg taggaagtgt 4140
 gcaaagttac gcctttggag atatgatgtg tgagacctgt agggaatgcg ttggagctca 4200
 aactctgtaa aatccctatt atagggacac agagtggaga ccaaactctc cctacgggca 4260
 acatcagcct aggaagccca atcgtcttta gcggttgggc acttcacctt aaaatatccc 4320
 gacagacact aacgaaaggc tttgttcttt aaagtctgca tggatatttc ctaccccaaa 4380
 aagacttaac cctttgctta aaattaagtt tgattgtgct agtgggttcg tgctatagtg 4440
 cgaaaattaa ttaaggggta taaagagagc ataaactaga aaaaacaagt agctataaca 4500
 aagatcaagt tcaaaaaatc atagagcttt tagagcaaat tgatcgcgct cttaacccaa 4560
 gaaaaatcag aaaaaccata ggaattatca caccttataa tgcccaaaaa agacgcttgc 4620
 gatcagaagt ggaaaaatac ggcttcaaga attttgatga gctcaaaata gacactgtgg 4680
 atgcctttca aggtgaagag gcagatatta ttattttattc caccgtgaaa acttgtggta 4740
 atctttcttt cttgctagat tctaaacgct tgaatgtggc tattttctagg gcaaaagaaa 4800
 atctcatttt tgtgggtaaa aagtctttct ttgagaattt atgaagcgat gagaagaata 4860
 tcttttagcg tattttgcaa gtctgtagat aggtaatctt ttccaaagat aatcattaga 4920
 cattcttcgc ttcaaaacgc tttcataaat ctctctaaag cgctttataa tcaacacaat 4980
 acccttatag tgtgagctat agcccctttt tgggaattga gttattttga ctttaaat 5040
 ttattagcgt tacaatttga gccattcttt agcttgtttt tctagccaga tcacatcgcc 5100
 gctcgcatga aattccactt tagggaatgc gtgtgcattt tttttaaggc cgtatttttg 5160
 ctgcaaatat cctacaatag catcgcccgat atggatgagt aggggggggtg ttgaaagggc 5220
 aaaatgctcc ataaaatagc cctcaatttt ttgagcgatt aagggaaaat gcgtgcaacc 5280
 taaaataatc acttcgggaa aatctttaag ggagtgaat aataacgcat gcaagtttct 5340
 aacaattcgc cctctaaaat actttcttca atcaaaggca caaaaagaga agtggctaaa 5400
 tgcgaaacat tcaaatagcc ttgttggttc agggcattgt cataagcgtt ggattggatc 5460
 gtcgcttttg tccctagcac taaaataggc gcgtttttat cttttacttg tcgcttgatc 5520
 gctaaaatgc ttggctcaat cagcccccac atagggattt tggaatgctt ttgcatctct 5580
 tctaaagcta gagcgctcgc tgtgttgcat gccacaatca ataattcaat ctggtgcggt 5640
 ttgaaaaaat ccaaagcctc taagccaaat tgcttgatcg tagtggggtc tttagtcca 5700
 taaggcactc tagccgtatc gccataatag atgatttcat caaataattg cgcttttaaa 5760
 aggcttttta aaacgctaaa ccctcccaca ccgctatcaa aaacgcctat tttcatgaca 5820

cttttttaaat ttaatgggat taattagga ttttattttt cattcattaa gtttaaaaaat 5880

tcttcattgt ccttagtttg ttgcatttta gaatagacaa agctt 5925

<210> 5

<211> 1147

<212> PRT

<213> Helicobacter pylori

<400> 5

Met Thr Asn Glu Thr Ile Asp Gln Gln Pro Gln Thr Glu Ala Ala Phe
1 5 10 15

Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val
20 25 30

Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp
35 40 45

Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu
50 55 60

Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
65 70 75 80

Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys
85 90 95

Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe
100 105 110

Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn
115 120 125

Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn
130 135 140

Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu
145 150 155 160

Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile
165 170 175

Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu
180 185 190

Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu
195 200 205

Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val
210 215 220

Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Ile
225 230 235 240

Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro Pro Glu Ala Arg Asp

245

250

255

Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met
260 265 270

Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys
275 280 285

Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met
290 295 300

Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly
305 310 315 320

Gly Asn Gly Gly Pro Gly Ala Arg His Asp Trp Asn Ala Thr Val Gly
325 330 335

Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His
340 345 350

Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile
355 360 365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser
370 375 380

Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Ile Asp Phe Met
385 390 395 400

Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys
405 410 415

Glu Lys Glu Lys Phe Arg Thr Glu Ile Lys Asp Phe Gln Lys Asp Ser
420 425 430

Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser
435 440 445

Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly
450 455 460

Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala
465 470 475 480

Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly Ser Leu Lys His Asp
485 490 495

Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser
500 505 510

Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu
515 520 525

Glu Val Gly Phe Asn Lys Val Ala Ile Phe Asn Leu Pro Asp Leu Asn
530 535 540

Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn Leu Glu Asp Lys Leu
545 550 555 560

Thr Thr Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Ile Lys Asp
565 570 575

Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Thr Leu Asn Phe Asn
580 585 590

Lys Ala Val Ala Asp Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys
595 600 605

Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg Lys Arg Glu His Leu
610 615 620

Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn
625 630 635 640

Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe
645 650 655

Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr
660 665 670

Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu
675 680 685

Asn Val Asn Lys Asn Leu Lys Asp Phe Asp Lys Ser Phe Asp Glu Phe
690 695 700

Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys
705 710 715 720

Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile
725 730 735

Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly
740 745 750

Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu
755 760 765

Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr Asp Lys Val
770 775 780

Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe
785 790 795 800

Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu
805 810 815

Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Ser Leu Asn Ala Arg Lys
820 825 830

Lys Ser Glu Ile Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu
835 840 845

Val Gly Asn Gly Leu Ser Gln Ala Glu Ala Thr Thr Leu Ser Lys Asn
850 855 860

Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn
865 870 875 880

Asn Asn Asn Asn Asn Gly Leu Lys Asn Glu Pro Ile Tyr Ala Lys Val
885 890 895

Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Leu Glu Glu Pro Ile Tyr
900 905 910

Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg Leu Asn Gln
915 920 925

Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Ala Gly Phe Pro Leu
930 935 940

Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg
945 950 955 960

Asn Gln Glu Leu Ala Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser
965 970 975

Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys
980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser
995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr
1010 1015 1020

Ala Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly
1025 1030 1035

Ala Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro
1040 1045 1050

Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val
1055 1060 1065

Gly Ser Val Pro Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln
1070 1075 1080

Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys
1085 1090 1095

Leu Asn Asn Ala Val Lys Asp Thr Asn Ser Gly Phe Thr Gln Phe
1100 1105 1110

Leu Thr Asn Ala Phe Ser Thr Ala Ser Tyr Tyr Cys Leu Ala Arg
1115 1120 1125

Glu Asn Ala Glu His Gly Ile Lys Asn Val Asn Thr Lys Gly Gly
1130 1135 1140

Phe Gln Lys Ser
1145

<210> 6
<211> 546
<212> PRT
<213> Helicobacter pylori

<400> 6

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
20 25 30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
35 40 45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
50 55 60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr
65 70 75 80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr
85 90 95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro
100 105 110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn
115 120 125

Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr
130 135 140

Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu
145 150 155 160

Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val
165 170 175

Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met
180 185 190

Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu
195 200 205

Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys
210 215 220

Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met
225 230 235 240

Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu
245 250 255

Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile
260 265 270

Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu
275 280 285

Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
290 295 300

Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly
305 310 315 320

Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly
325 330 335

His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile
340 345 350

Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu
355 360 365

Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
370 375 380

Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser
385 390 395 400

Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala
405 410 415

Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp
420 425 430

Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu
435 440 445

Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn
450 455 460

Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly
465 470 475 480

Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val
485 490 495

Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu
500 505 510

Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro
515 520 525

Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly
530 535 540

Met Met
545

<210> 7
<211> 1838
<212> DNA
<213> Helicobacter pylori

<400> 7
aagcttgctg tcatgatcac aaaaaacact aaaaaacatt attattaagg atacaaaatg 60
gcaaaagaaa tcaaattttc agatagtgcg agaaaccttt tatttgaagg cgtgaggcaa 120
ctccatgacg ctgtcaaagt aaccatgggg ccaagaggca ggaatgtatt gatccaaaaa 180
agctatggcg ctccaagcat caccaaagac ggcgtgagcg tggctaaaga gattgaatta 240
agttgcccag tagctaacat gggcgctcaa ctcggttaaag aagtagcgag caaaaccgct 300
gatgctgccg gcgatggcac gaccacagcg accgtgctag cttatagcat ttttaaagaa 360
ggtttgagga atatcacggc tggggctaac cctattgaag tgaaacgagg catggataaa 420
gctgctgaag cgatcattaa tgagcttaaa aaagcgagca aaaaagtagg cggtaaagaa 480
gaaatcacc c aagtggcgac catttctgca aactccgatc acaatatcgg gaaactcatc 540
gctgacgcta tggaaaaagt gggtaaagac ggcgtgatca ccgttgagga agctaagggc 600
attgaagatg aattggatgt cgtagaaggc atgcaatttg atagaggcta cctctcccct 660
tattttgtaa cgaacgctga gaaaatgacc gctcaattgg ataatgctta catcctttta 720
acggataaaa aaatctctag catgaaagac attctccgc tactagaaaa aaccatgaaa 780
gagggcaaac cgcttttaaat catcgctgaa gacattgagg gcgaagcttt aacgactcta 840
gtggtgaata aattaagagg cgtgttgaat atcgcgagcg ttaaagctcc aggctttggg 900
gacagaagaa aagaaatgct caaagacatc gctattttta ccggcggtca agtcattagc 960
gaagaattgg gcttgagtct agaaaacgct gaagtggagt ttttaggcaa agctggaagg 1020
attgtgattg acaaagacaa caccacgatc gtagatggca aaggccatag cgatgatgtt 1080
aaagacagag tcgcgcagat caaaacccaa attgcaagta cgacaagcga ttatgacaaa 1140
gaaaaattgc aagaaagatt ggctaaactc tctggcggtg tggctgtgat taaagtgggc 1200
gctgcgagtg aagtggaaat gaaagagaaa aaagaccggg tggatgacgc gttgagcgcg 1260
actaaagcgg cggttgaaga aggcattgtg attggtggcg gtgcggctct cattcgcgcg 1320
gctcaaaaag tgcatttgaa tttgcacgat gatgaaaaag tgggctatga aatcatcatg 1380
cgcgccatta aagccccatt agctcaaact gctatcaacg ctggttatga tggcgggtgtg 1440
gtcgtgaatg aagtagaaaa acacgaaggg catttttggt ttaacgctag caatggcaag 1500
tatgtggata tgtttaaaga aggcattatt gacccttaa aagtagaaag gatcgctcta 1560
caaaatgcgg tttcggtttc aagcctgctt ttaaccacag aagccaccgt gcatgaaatc 1620

aaagaagaaa aagcgactcc ggcaatgcct gatatgggtg gcatgggcgg tatgggaggc 1680
atgggcggca tgatgtaagc ccgcttgctt tttagtataa tctgctttta aaatcccttc 1740
tctaaatccc cccctttcta aaatctcttt tttggggggg tgctttgata aaaccgctcg 1800
cttgtaaaaa catgcaacaa aaaatctctg ttaagctt 1838

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer Oligonucleotide

<400> 8
gactcgagtc gacatcga 18

B2

<210> 9
<211> 12
<212> PRT
<213> Helicobacter pylori
<400> 9

Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys
1 5 10

<210> 10
<211> 5
<212> PRT
<213> Helicobacter pylori
<400> 10

Glu Pro Ile Tyr Ala
1 5